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Substitute for form 1449A/PTO <b>INFORMATION DISCLOSURE STATEMENT BY APPLICANT</b> <i>(Use as many sheets as necessary)</i>			<b>Complete if Known</b> Application Number 10/032,281 Filing Date December 21, 2001 First Named Inventor WYRICK, JOHN Art Unit 1637 Examiner Name Horlick, Kenneth R Attorney Docket Number WTHD-007CIP	
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FOREIGN PATENT DOCUMENTS						
Examiner Initials <sup>5</sup>	Cite No. <sup>1</sup>	Foreign Patent Document	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T <sup>6</sup>
		Country Code <sup>2</sup> Number <sup>3</sup> Kind Code <sup>4</sup> (if known)				

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		Art Unit	1637		
		Examiner Name	Horlick, Kenneth R		
Sheet	2	of	3	Attorney Docket Number	WTHD-007CIP

## NON PATENT LITERATURE DOCUMENTS

Examiner Initials*	Cite No. <sup>1</sup>	Include name of the author (in CAPITAL LETTERS); title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T <sup>2</sup>
/KH/		BARNARD, et al. PCR bias toward the wild-type k-ras and p53 sequences: Implications for PCR detection of mutations and cancer diagnosis. <i>BioTechniques</i> . 1998, vol. 25, no. 4, pp 684-691.	
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		Ji, et al. Preservation of gene expression ratios among multiple complex cDNAs after PCR amplification: Application to differential gene expression studies. <i>Journal of Structural and Functional Genomics</i> . 2000, vol. 1, pp. 1-7.	
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		LOCKHART, et al. Genomics, gene expression and DNA arrays. <i>Nature</i> . 2000, vol. 405, pp. 827-836.	
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		MATHIEU-DAUDE, et al. DNA rehybridization during PCR: the 'C <sub>0</sub> t' effect' and its consequences. <i>Nucleic Acids Research</i> . 1996, vol. 24, no. 11, pp. 2080-2086.	
		POLZ, et al. Bias in template-to-product ratios in multitemplate PCR. <i>Applied and Environmental Microbiology</i> . 1998, vol. 64, pp. 3724-3730.	
/KH/		SCHWABE, et al. High-copy cDNA amplification of minimal total RNA quantities for gene expression analyses. <i>Molecular Biotechnology</i> . 2000, vol. 14, pp. 165-172.	

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/KH/		SUZUKI, et al. Kinetic bias in estimates of coastal picoplankton community structure obtained by measurements of small-subunit rRNA gene PCR amplicon length heterogeneity. Applied and Environmental Microbiology. 1998, vol. 64, no. 11, pp. 4522-4529.	
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/KH/		WINTZINGERODE, et al. Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. FEMS Microbiology Reviews. 1997, vol. 21, pp. 213-229.	
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